

STATUS OF CLAIMS:

1. (Currently amended) A method for improving the reliability of physical measurements obtained from array hybridization studies performed on an array having a ~~large~~first number of genomic samples, each composed of a ~~small~~ number of replicates insufficient for making precise and valid statistical inferences, the number of replicates being less than the first number, comprising the step of estimating an error in measurement of a selected sample by averaging errors obtained when measuring at least one of the ~~large~~first number of samples and a subset of the large number of samples, and utilizing the estimated sample error as a standard for accepting or rejecting the measurement of the ~~respective~~selected sample.

2. (Currently amended) The method of claim 1 wherein a physical measurement quantity is determined based on ~~the~~a difference between statistically dependent quantities.

3. (Currently amended) The method of claim 1 wherein a physical measurement quantity determined from an entire array population is used to estimate discrete instances of that quantity for the ~~small~~ number of replicate samples within that population.

4. (Previously presented) The method of claim 1 wherein the estimates of measurement error are used to plan, manage and control array hybridization studies on the basis of (a) the probability of detecting a true difference of specified magnitude between physical measurements of a given number of replicates, or (b) the number of replicates required to detect a true difference of specified magnitude.

5. (Withdrawn) A method for improving the reliability and accuracy of the physical measurements obtained from array hybridization studies performed on an array having a large number of genomic samples, each composed of a small number of replicates insufficient for making precise and valid statistical inferences, comprising the step of detecting outlier values in the

